

STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/542,937
Source: PG/10
Date Processed by STIC: 7/29/05

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.2.2 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail. Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom. Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05): U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/24/05

BEST AVAILABLE COPY

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER:

10/542,937

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics
 Wrapped Aminos The number/text at the end of each line “wrapped” down to the next line. This may occur if your file was retrieved in a word processor **after** creating it. Please adjust your right margin to .3; this will prevent “wrapping.”
 - 2 Invalid Line Length The rules require that a line **not exceed** 72 characters in length. This includes white spaces.
 - 3 Misaligned Amino
 Numbering The numbering under each 5th amino acid is misaligned. Do **not** use tab codes between numbers; use **space characters**, instead.
 - 4 Non-ASCII The submitted file was **not** saved in ASCII(DOS) text, as **required** by the Sequence Rules. Please **ensure your subsequent submission is saved in ASCII text**.
 - 5 Variable Length Sequence(s) contain n’s or Xaa’s representing more than one residue. **Per Sequence Rules, each n or Xaa can only represent a single residue.** Please present the **maximum** number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
 - 6 PatentIn 2.0
 “bug” A “bug” in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**
 - 7 Skipped Sequences Sequence(s) missing. If intentional, please insert the following lines for **each** skipped sequence:
 (OLD RULES) (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where “X” is shown)
 (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
 (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where “X” is shown)
 This sequence is intentionally skipped

 Please also adjust the “(ii) NUMBER OF SEQUENCES:” response to **include** the skipped sequences.
 - 8 Skipped Sequences Sequence(s) missing. If **intentional**, please insert the following lines for **each** skipped sequence.
 (NEW RULES) <210> sequence id number
 <400> sequence id number
 000
 - 9 Use of n’s or Xaa’s Use of n’s and/or Xaa’s have been detected in the Sequence Listing.
 (NEW RULES) Per 1.823 of Sequence Rules, use of <220>-<223> is **MANDATORY** if n’s or Xaa’s are present.
 In <220> to <223> section, please explain location of **n** or **Xaa**, and which residue **n** or **Xaa** represents.
 - 10 Invalid <213> Per 1.823 of Sequence Rules, the only **valid** <213> responses are: Unknown, Artificial Sequence, or
 Response scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or is Artificial Sequence
 - 11 Use of <220> ~~Sequence(s) missing the <220> “Feature” and associated numeric identifiers and responses.~~
 Use of <220> to <223> is **MANDATORY** if <213> “Organism” response is “Artificial Sequence” or
 “Unknown.” Please explain source of genetic material in <220> to <223> section.
 (See “Federal Register,” 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
 - 12 PatentIn 2.0 Please do not use “Copy to Disk” function of PatentIn version 2.0. This causes a corrupted file,
 “bug” resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use “File Manager” or any other manual means to copy file to floppy disk.
 - 13 Misuse of n/Xaa “n” can **only** represent a single nucleotide; “Xaa” can **only** represent a single amino acid



PCT

IMPORTANT! see
item 4 on Enor
summary sheet

Do NOT
use bold
print

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/542,937

DATE: 07/29/2005
TIME: 08:45:53

Input Set : A:\PTO.RJ.txt
Output Set : N:\CRF4\07292005\J542937.raw

see
pp 1-4

3 <110> APPLICANT: EFARMES, S.A.
W--> 4 <120> TITLE OF INVENTION: Device a meted for detecting low density lipoprotein
receptor gene
W--> 5 mutations
W--> 6 associated with familial hypercholesterolemia
W--> 7 <130> FILE REFERENCE: PCT-154
C--> 8 <140> CURRENT APPLICATION NUMBER: US/10/542,937
C--> 8 <141> CURRENT FILING DATE: 2005-07-21
W--> 8 <160> NUMBER OF SEQ ID: 259
W--> 9 <150> PRIOR APPLICATION NUMBER: ES200300206
W--> 10 <151> PRIOR FILING DATE: 28.01.03 2003-01-28
W--> 11 <150> PRIOR APPLICATION NUMBER: ES200302671
W--> 12 <151> PRIOR FILING DATE: 17.11.03 2003-11-17

do you mean "method"?

use this date format
Does Not Comply
Formatted Diskette Needs

ERRORED SEQUENCES

E--> 13 <210> SEQ ID NO: 1
14 <211> LENGTH: 60.000
E--> 15 <212> TYPE: polynucleotide
16 <213> ORGANISM: human
W--> 17 <220> FEATURE:
18 <221> NAME/KEY: gene
19 <223> OTHER INFORMATION: rLDL
W--> 20 <400> SEQUENCE: 16 insert the sequence number
22 aaaagatggt gtatccattc aatggaacat tatttggcct ttaaaaggaa ggaaattctc 60
23 actgagcata gtggtttatg cctgtaatcc cagcactttg ggaggctgag gcagggggga 120
24 gggggcggtt cacctgaggt caggagttca agaccagcct ggccaacatg gtgaaatccc 180
25 gtctctacta aaaatacaaa aaaattagcc gagtgtggtg gcacacacct gtaagccagg 240
26 ctacacggga gactgaggca ggagaatcgc tggaaaccgg gaggcagagg ctgcagagag 300
27 ccgagattgc gtcactgcac tccagcctgg gtgacagagc gagactcttg tcttaaaaaa 360
28 aaaaagaagg aaggaaggaa ggaaggagg aagttctgac acaggctcca acacagatgt 420
29 tatgctcagt gaaataagcc agacatgaaa ggacaaatac tgctgatct cattcataag 480
30 aggtccctag aattgtagaa tgggtgtgtg cacgggctgg gagggggtgt ggccagagtt 540
31 tcagtttggg aagttgagaa tgttctggag atggatggcg gtatgggtgg ttgcacaact 600
32 gtgtgaatgc gcttaatgcc tctgaattgt gcagttacaa gtggttcgga tgggccgggc 660
33 gcggtggtct atgcctgtaa tcccagcact ttgggaggcc gaggcaggtg gatcatgaga 720
34 tcaggagatc gagaccatcc tggctaacac ggtgaaaccc catctctact aaaaaataca 780
35 aaaaattagc caggcatggt ggtgggcacc tgtagtccca gctacttggg aggcggaggc 840
36 aggagaatgg cgtgaacacg ggaggcagaa cttgcagtga gccgagatca cgccactgca 900
37 ctccagcctg ggcgacagag tgagactccg tctaaaaaaa aaaaagtggg taagatgggc 960
38 cgggcatggg ggatcacgct tgcaatccca acactttggg aggctgaggt ggggtgattac 1020
39 gaggtcagga gttcgagacc agcctgacca ccatggtgaa accccgtctc tactaaaagt 1080
40 acaaaattag ccgggtgtcg tggcacacgt ctgtaatccc agctactggg gaggctgagt 1140

do NOT use alphabetical headings

inhib response. The only valid
<212> responses
are DNA,
RNA, or
PRT

2

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/542,937

DATE: 07/29/2005

TIME: 08:45:53

Input Set : A:\PTO.RJ.txt

Output Set: N:\CRF4\07292005\J542937.raw

```

237 tgetttaagt tgaatcttta aacttatctt tatttttgag acacagtctc actctgtcgc 12960
238 ccaggctgga gtgcagtggg acaaccacag ctgagtgcag cgttgacctc ctgggctcaa 13020
239 gccatcctcc cgccctcagcc tcccagtag ctgggactac aggcgcacac aacctgtcc 13080
240 agcttatttt tgtatttttt gtagagacag ggtccactg tgttgccctg gcttgctctg 13140
241 aactcctagg ctcaagtgat cccccgcct caccctccca aagtgtctggg attacaggca 13200
242 tgagccacca catccagact tcaacttttt gttaaatgtc gcaaagtggc taaggaatgg 13260
243 gattcaatgg ggacacattt ataaacgttg cagcagctcc tagaacttgc ctatccttgt 13320
244 aaacttctct aggtgattgc taattacttc tttttttttt tttttttttg agacggagtc 13380
245 tcaactctgt gccccaggct gagtacagt ggcgaatctc gtctcactgc aaactccacc 13440
246 tcccgggttc acgccattct cctgcctcag cctcccgagt agctgggact acaggcacc 13500
247 gccaccacgc ccggctaatt ttttgtattt ttttttagta gaggtggggg ttcactgtgt 13560
248 tatccaggat ggtcttgatc tctgcacctc gtgatccacc tgcctcagcc tcccaaagt 13620
249 ctgggattac aggcgtgagc caccatgccc agcccgttaa ttatttcaat ttgacctga 13680
250 cactgagcct gccaaagttag ttcaagcatt ttgatggccc ctttacaggg tgggaaagt 13740
251 aatttatctg tccaaggccg aattctgaaa ctgagtctta actgccaaa attcttaca 13800
252 tcaatttctt cttctgggtt gggcacagt gctcatgcct gtaaagccag caatttgaga 13860
253 ggcatcatga tgcaagagga agaggattga gtgaagctag gagtttggga ccagcctggg 13920
254 caacatagt agaccccatc tataaaaaaa aattaaaaat tagttgggca tgggtggtgca 13980
255 ctctgtggt cctagctatt caggaggtcg aggtgggagg attccttgag cccagggttg 14040
256 acgtgcaga gagctgtgat cagccactg cagtcagcc tgagtgcag ctggaaataa 14100
257 tgataaataa ataataaata attattttaa aaattataat aaaaataatt aaaaattat 14160
258 tttccctgat taatcttttt tttgtcctt ctgagagttc aatttgtccc tttctgcct 14220
259 ggtctcctag gtttccctaa aatcctgctg agagggttagc actgcctgcc aaagtcagtt 14280
260 tgcaaaatcc cagagaaatc cagcttattc ctgggggaac cgccaagact gccagccct 14340
261 gtgtgggggt caggcaagtt tctcacatgt gccttttttg caagaggcct ctggcaaccc 14400
262 catgagtcct caaagagact caattctaaa agttggtctc caccagctct ctgtggctta 14460
263 ggggttcaag ttcaactgtg aaagccctgt tttgttttga ttttgccttg agggagagga 14520
264 aaccgccctt ctgtttgttc aactccttct cctaagggga gaaatcaata tttacgtcca 14580
265 gactccagg atccgtacaa ttgatttttc agatgtttat actcagccaa aggcgggatc 14640
266 ccacaaaaca aaaaatattt ttttggctgt acttttgtga agattttatt taaattcctg 14700
267 gaagctacgt gtcattaggg tgatttggaa taacaatgta aaaacaatat acaacgaaag 14760
268 aaagctaaaa atctatacac aattcctaga aaggaaaagg caaatataga aagtggcggg 14820
269 agttcccaac attttttagtg ttttctttt gaggcagaga ggacaatggc attaggttat 14880
270 tggaggatct tgaaaggctg ttgttatcct tctgtggaca acaacagcaa aatgttaaca 14940
271 gttaaacatc gagaaatttc agggagatct ttcagaagat gcgtttccaa ttttgagggg 15000
272 gcgtcagctc ttcaccggag acccaaatac aacaaatcaa gtcgcctgcc ctggcgacac 15060
273 tttcgaagga ctggagtggg aatcagagct tcacgggtta aaaagccgat gtcacatcgg 15120
274 ccgttcgaaa ctctcctct tgcagtgagg tgaagacatt tgaaaatcac cccactgcaa 15180
275 actcctcccc ctgctagaaa cctcacattg aaatgctgta aatgacgtgg gccccgagt 15240
276 caatcgcggg aagccagggt tccagctag gacacagcag gtcgtgatcc gggtcgggac 15300
277 actgcctggc agaggtgctg agc atg ggg ccc tgg ggc tgg aaa ttg cgc 15350
278 met met gly pro trp gly trp lys leu arg ← these are misaligned. They
279 -21 -20 -15 need to be directly
280 tgg acc gtc gcc ttg ctg ctg gcc gcg gcg ggg act qca g gtaaggcttg 15400
281 trp thr val ala leu leu leu ala ala ala gly thr ala v
282 -10 -5 -1 1 under
283 ctccaggcgc cagaataggg tgagaggagg cccccgggg gcccttgagg atttattttt 15460
284 ttgggtacaa ataactcctc catccctggg agacttgtgg ggtaatggca cggggtcctt 15520
285 cccaaacggc tggagggggg gctggagggg ggcgtgagg ggagcgcgag ggtcgggagg 15580

```

use upper-case for initial letter of amino acid

Met Gly Pro

They need to be directly under codon atg met

do not use TAB codes between 7/29/05 amino acids

RAW SEQUENCE LISTING

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Input Set : A:\PTO.RJ.txt

Output Set: N:\CRF4\07292005\J542937.raw

1176 agtagctggg gccacaggcg cctgccacca cgcccggtta attttttttt gtacttcttt 59327
1177 tagtacagac ggggtttcac catgttagcc aggatggtct cgatctctg accttgat 59387
1178 ccacctgctt cggcctccca aagtgtgag attacaggcg tgagccaccg cgggtggcca 59447
1179 acgctaattt tttgttttt ttagatggag tcttgctctg tcgcccaggc tggagtgcag 59507
1180 tggcgtgac tctgcctact gcaagctccg cctcccggt tcatgccatt ctctgcctc 59567
1181 agcctcctga gtaactggga ctacaggcac ccgccaccac gcccggttaa ttttttgtat 59627
1182 ttttagtaga gacagggttt caccgtgtta gccaggatgg tcttgatctc ctgacctgt 59687
1183 gatccacccg tctcggcctc ccaaagtgt gggattagag gtgtgagcca ccacacctgg 59747
1184 cctagcctgg ctaatttttg tatttttggg agagacgggg ttccaccatg ttggtcaggc 59807
1185 tggctctgaa cttctgacct caggtaatct gcctgcctca gtctcccaaa gtgctgggat 59867
1186 tacagggtgt agccaccgcg cctggcctca ctctctctg tcatctgttt gtggattgga 59927
1187 ctccccagga gaaggaccca gaagggaag actccagaa ctccgggcaa gatgcaatct 59987
1188 ccgtgggctg cca 60000

E--> 1190 <210> ~~SEQ ID NO: 2~~
1191 <211> LENGTH: 24
E--> 1192 <212> TYPE: polynucleotide
1193 <213> ORGANISM: artificial sequence
W--> 1194 <220> FEATURE:
W--> 1195 <221> NAME/KEY: oligonucleotide
1196 <223> OTHER INFORMATION: Ex1F
W--> 1197 <400> SEQUENCE: 24 insert
1198 cacttgaaa tgctgtaaa gacg
E--> 1200 <210> SEQ ID NO: SEQ ID NO: 3
1201 <211> LENGTH: 24
E--> 1202 <212> TYPE: polynucleotide
1203 <213> ORGANISM: artificial sequence
W--> 1204 <220> FEATURE:
W--> 1205 <221> NAME/KEY: oligonucleotide
1206 <223> OTHER INFORMATION: Ex1R
E--> 1209 <400> SEQUENCE:
1210 ctattctggc gcctggagca agcc
E--> 1212 <210> SEQ ID NO: SEQ ID NO: 4
1213 <211> LENGTH: 24
E--> 1214 <212> TYPE: polynucleotide
1215 <213> ORGANISM: artificial sequence
W--> 1216 <220> FEATURE:
W--> 1217 <221> NAME/KEY: oligonucleotide
1218 <223> OTHER INFORMATION: Ex2F
W--> 1219 <400> SEQUENCE:
1220 ttgagagacc ctttctcctt ttcc
E--> 1222 <210> SEQ ID NO: SEQ ID NO: 5
1223 <211> LENGTH: 20
E--> 1224 <212> TYPE: polynucleotide
1225 <213> ORGANISM: artificial sequence
W--> 1226 <220> FEATURE:
W--> 1227 <221> NAME/KEY: oligonucleotide
1228 <223> OTHER INFORMATION: Ex2R
W--> 1229 <400> SEQUENCE:
1230 gcatatcatg cccaaagggg

*delete**invalid*

*give source of genetic material
(see item 11 on
Error summary
sheet)*

*24 ← insert
cumulative
base total
at right
margin of
each line*

*fix
these
errors*

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/542,937

DATE: 07/29/2005
TIME: 08:45:53

4

Input Set : A:\PTO.RJ.txt
Output Set: N:\CRF4\07292005\J542937.raw

E--> 1506 <212> TYPE: polynucleotide
1507 <213> ORGANISM: artificial sequence
W--> 1508 <220> FEATURE:
W--> 1509 <221> NAME/KEY: oligonucleotide
1510 <223> OTHER INFORMATION: Ex15R
W--> 1511 <400> SEQUENCE:
1512 tagggagggc ccagtcttt
E--> 1514 <210> SEQ ID NO: SEQ ID NO: 34
1515 <211> LENGTH: 20
E--> 1516 <212> TYPE: polynucleotide
1517 <213> ORGANISM: artificial sequence
W--> 1518 <220> FEATURE:
W--> 1519 <221> NAME/KEY: oligonucleotide
1520 <223> OTHER INFORMATION: Ex17F
W--> 1521 <400> SEQUENCE:
1522 ggggtctctgg tctcgggggc
E--> 1524 <210> SEQ ID NO: SEQ ID NO: 35
1525 <211> LENGTH: 22
E--> 1526 <212> TYPE: polynucleotide
1527 <213> ORGANISM: artificial sequence
W--> 1528 <220> FEATURE:
W--> 1529 <221> NAME/KEY: oligonucleotide
1530 <223> OTHER INFORMATION: Ex17R
W--> 1531 <400> SEQUENCE:
1532 ggctctggct ttctagagag gg
E--> 1534 <210> SEQ ID NO: SEQ ID NO: 36
1535 <211> LENGTH: 23
E--> 1536 <212> TYPE: polynucleotide
1537 <213> ORGANISM: artificial sequence
W--> 1538 <220> FEATURE:
W--> 1539 <221> NAME/KEY: oligonucleotide
W--> 1540 <223> OTHER INFORMATION: *← mandatory response needed on <223> line*
W--> 1540 <400> SEQUENCE:
1541 cgggtcggga cactgcctgg cag
E--> 1544 <210> SEQ ID NO: SEQ ID NO: 37
1545 <211> LENGTH: 23
E--> 1546 <212> TYPE: polynucleotide
1547 <213> ORGANISM: artificial sequence
W--> 1548 <220> FEATURE:
W--> 1549 <221> NAME/KEY: oligonucleotide
W--> 1550 <223> OTHER INFORMATION:
W--> 1550 <400> SEQUENCE:
1551 cgggtcggga ccctgcctgg cag
E--> 1553 <210> SEQ ID NO: SEQ ID NO: 38
1554 <211> LENGTH: 23
E--> 1555 <212> TYPE: polynucleotide
1556 <213> ORGANISM: artificial sequence
W--> 1557 <220> FEATURE:
W--> 1558 <221> NAME/KEY: oligonucleotide

fix these errors

*Artificial Sequence MUST be
Explained on <223> line*

*These pages are
shown as samples of global
errors. Please consult Sequence
Rules and attached sample sequence
listing for valid format.*

<110> Smith, John; Smithgene Inc.

<120> Example of a Sequence Listing

<130> 01-00001

<140> PCT/EP98/00001

<141> 1998-12-31

<150> US 08/999,999

<151> 1997-10-15

<160> 4

<170> PatentIn version 2.0

<210> 1

<211> 389

<212> DNA

<213> Paramecium sp.

<220>

<221> CDS

<222> (279)...(389)

<300>

<301> Doe, Richard

<302> Isolation and Characterization of a Gene Encoding a
Protease from Paramecium sp.

Journal of Genes

<303> 1

<304> 4

<305> 1-7

<306> 1988-06-31

<307> 123456

<308> 1988-06-31

<400> 1

agctgtagtc	attcctgtgt	cctcttctct	ctgggcttct	caccctgcta	atcagatctc	60
agggagagtg	tcttgaccct	cctctgcctt	tgcagettca	caggcaggca	ggcaggcagc	120
tgatgtggca	attgctggca	gtgccacagg	cttttcagcc	aggcttaggg	tgggttcgcg	180
cgcggcgcg	cgccccctct	cgcgctctct	tcgcgcctct	ctctcgctct	cctctcgctc	240

Consult this

ggacctgatt aggtgagcag gaggaggggg cagttagc atg gtt tca atg ttc agc 296
Met Val Ser Met Phe Ser 5

ttg tct ttc aaa tgg cct gga ttt tgt ctg tct gtt tgt ttg ttc caa 344
Leu Ser Phe Lys Trp Pro Gly Phe Cys Leu Phe Val Cys Leu Phe Gln 20

tgt ccc aaa gtc ctc ccc tgt cac tca tca ctg cag ccg aat ctt 389
Cys Pro Lys Val Leu Pro Cys His Ser Ser Leu Gln Pro Asn Leu 25 30 35

<210> 2
<211> 37
<212> PRT
<213> Paramecium sp.

<400> 2
Met Val Ser Met Phe 5 Ser Leu Ser Phe Lys 10 Trp Pro Gly Phe Cys 15 Leu

Phe Val Cys Leu 20 Phe Gln Cys Pro Lys 25 Val Leu Pro Cys His 30 Ser Ser

Leu Gln Pro Asn Leu 35

<210> 3
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Designed peptide based on size and polarity to act as a linker between the alpha and beta chains of Protein XYZ.

<400> 3
Met Val Asn Leu Glu 5 Pro Met His Thr Glu 10 Ile

<210> 4
<400> 4
000

identifiers and their accompanying information as shown in the following table. The numeric identifier shall be used only in the "Sequence Listing." The order and presentation of the items of information in the "Sequence Listing" shall conform to the arrangement given below. Each item of information shall begin on a new line and shall begin with the numeric identifier enclosed in angle brackets as shown. The submission of those items of information designated with an "M" is mandatory. The submission of those items of information designated with an "O" is optional. Numeric identifiers <110> through <170> shall only be set forth at the beginning of the "Sequence Listing." The following table illustrates the numeric identifiers.

Numeric Identifier	Definition	Comments and Format	Mandatory (M) or Optional (O)
<110>	Applicant	Preferably max. of 10 names; one name per line; preferable format: Surname, Other Names and/or Initials	M
<120>	Title of Invention		M
<130>	File Reference	Personal file reference	M when filed prior to assignment of appl. number
<140>	Current Application Number	Specify as: US 07/999,999 or PCT/US96/99999	M, if available
<141>	Current Filing Date	Specify as: yyyy-mm-dd	M, if available
<150>	Prior Application Number	Specify as: US 07/999,999 or PCT/US96/99999	M, if applicable include priority documents under 35 USC 119 and 120
<151>	Prior Application Filing Date	Specify as: yyyy-mm-dd	M, if applicable
<160>	Number of SEQ ID NOs	Count includes total number of SEQ ID NOs	M
<170>	Software	Name of software used to create the Sequence Listing	O
<210>	SEQ ID NO:#:	Response shall be an integer representing the SEQ ID NO shown	M
<211>	Length	Respond with an integer expressing the number of bases or amino acid residues	M

<212>

Type

Whether presented
sequence mole-
cule is DNA,
RNA, or PRT
(protein). If
a nucleotide
sequence con-
tains both DNA
and RNA frag-
ments, the
type shall be
"DNA." In ad-
dition, the
combined DNA/
RNA molecule
shall be further
described in
the <220> to
<223> feature
section.

M

<213>

Organism

Scientific name,
i.e. Genus/species,
Unknown or Artifi-
cial Sequence. In
addition, the
"Unknown" or
"Artificial Se-
quence" organisms
shall be further
described in the
<220> to <223>
feature section.

M

<220>

Feature

Leave blank after
<220>. <221-223>
provide for a
description of
points of bio-
logical signi-
ficance in the
sequence.

M, under the
following condi-
tions: if "n,"
"Xaa," or a mod-
ified or unusual
L-amino acid or
modified base was
used in a se-
quence; if ORGAN-
ISM is "Artifi-
cial Sequence" or
"Unknown"; if
molecule is
combined DNA/RNA.

<221>

Name/Key

Provide appropriate
identifier for
feature, pre-
ferably from
WIPO Standard
ST.25 (1998),
Appendix 2,
Tables 5 and 6

M, under the fol-
lowing conditions:
if "n," "Xaa," or
a modified or un-
usual L-amino
acid or modified
base was used in
a sequence

<222>

Location

Specify location
within sequence;
where appropriate
state number of
first and last
bases/amino acids

M, under the fol-
lowing conditions:
if "n," "Xaa," or
a modified or un-
usual L-amino
acid or modified

		In feature	base was used in a sequence
<223>	Other information	Other relevant information; four lines maximum	M, under the following conditions: if "n," "Xaa," or a modified or unusual L-amino acid or modified base was used in a sequence; if ORGANISM is "Artificial Sequence" or "Unknown"; if molecule is combined DNA/RNA.
<300>	Publication Information	Leave blank after <300>	0
<301>	Authors	Preferably max of ten named authors of publication; specify one name per line; preferable format: Surname, Other Names and/or Initials	0
<302>	Title		0
<303>	Journal		0
<304>	Volume		0
<305>	Issue		0
<306>	Pages		0
<307>	Date	Journal date on which data published; specify as yyyy-mm-dd, MMM-yyyy or Season-yyyy	0
<308>	Database Accession Number	Accession number assigned by database including database name	0
<309>	Database Entry Date	Date of entry in database; specify as yyyy-mm-dd or MMM-yyyy	0
<310>	Patent Document Number	Document number; for patent-type citations only. Specify as, for example, US 07/999,999	0

<311>

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DateDocument Filing
date, for patent-
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specify as yyyy-mm-dd

0

<312>

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Document publication
date, for
patent-type
citations only;
specify as yyyy-mm-dd

0

<313>

Relevant
ResiduesFROM (position) TO
(position)

0

<400>

Sequence

SEQ ID NO should
follow the
numeric identifier
and should appear
on the line pre-
ceding the actual
sequence

M

5. Section 1.824 is revised to read as follows:

1.824 Form and format for nucleotide and/or amino acid sequence submissions in computer readable form.

(a) The computer readable form required by 1.821(e) shall meet the following specifications:

(1) The computer readable form shall contain a single "Sequence Listing" as either a diskette, series of diskettes, or other permissible media outlined in paragraph (c) of this section.

(2) The "Sequence Listing" in paragraph (a) (1) of this section shall be submitted in American Standard Code for Information Interchange (ASCII) text. No other formats shall be allowed.

(3) The computer readable form may be created by any means, such as word processors, nucleotide/amino acid sequence editors or other custom computer programs; however, it shall conform to all specifications detailed in this section.

(4) File compression is acceptable when using diskette media, so long as the compressed file is in a self-extracting format that will decompress on one of the systems described in paragraph (b) of this section.

(5) Page numbering shall not appear within the computer readable form version of the "Sequence Listing" file.

(6) All computer readable forms shall have a label permanently affixed thereto on which has been hand-printed or typed: the name of the applicant, the title of the invention, the date on which the data were recorded on the computer readable form, the operating system used, a reference number, and an application serial number and filing date, if known.

(b) Computer readable form submissions must meet these format requirements:

(1) Computer: IBM PC/XT/AT, or compatibles, or Apple Macintosh;

(2) Operating System: MS-DOS, Unix or Macintosh;

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